



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/735,972

DATE: 08/05/2004

TIME: 12:31:21

Input Set : A:\07917-198001.TXT

Output Set: N:\CRF4\08052004\J735972.raw

4 <110> APPLICANT: Pereira, Andrea
 5 Wentworth, Diana Bilodeau
 6 Gandhi, Rita
 8 <120> TITLE OF INVENTION: KINESIN-LIKE PROTEINS AND METHODS OF USE
 11 <130> FILE REFERENCE: 07917-198001
 13 <140> CURRENT APPLICATION NUMBER: US 10/735,972
 14 <141> CURRENT FILING DATE: 2003-12-15
 16 <150> PRIOR APPLICATION NUMBER: US 60/433,098
 17 <151> PRIOR FILING DATE: 2002-12-13
 19 <160> NUMBER OF SEQ ID NOS: 16
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2697
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)...(2694)
 32 <400> SEQUENCE: 1



33	atg tct gtc act gag gaa gac ctg tgc cac cat atg aaa gta gta gtt	48
34	Met Ser Val Thr Glu Glu Asp Leu Cys His His Met Lys Val Val Val	
35	1 5 10 15	
37	cgt gta cgt ccg gaa aac act aaa gaa aaa gca gct gga ttt cat aaa	96
38	Arg Val Arg Pro Glu Asn Thr Lys Glu Lys Ala Ala Gly Phe His Lys	
39	20 25 30	
41	gtg gtt cat gtt gtg gat aaa cat atc cta gtt ttt gat ccc aaa caa	144
42	Val Val His Val Val Asp Lys His Ile Leu Val Phe Asp Pro Lys Gln	
43	35 40 45	
45	gaa gaa gtc agt ttt ttc cat gga aag aaa act aca aat caa aat gtt	192
46	Glu Glu Val Ser Phe Phe His Gly Lys Lys Thr Thr Asn Gln Asn Val	
47	50 55 60	
49	ata aag aaa caa aat aag gat ctt aaa ttt gta ttt gat gct gtt ttt	240
50	Ile Lys Lys Gln Asn Lys Asp Leu Lys Phe Val Phe Asp Ala Val Phe	
51	65 70 75 80	
53	gat gaa acg tca act cag tca gaa gtt ttt gaa cac act act aag cca	288
54	Asp Glu Thr Ser Thr Gln Ser Glu Val Phe Glu His Thr Thr Lys Pro	
55	85 90 95	
57	att ctt cgt agt ttt ttg aat gga tat aat tgc aca gta ctt gcc tat	336
58	Ile Leu Arg Ser Phe Leu Asn Gly Tyr Asn Cys Thr Val Leu Ala Tyr	
59	100 105 110	
61	ggt gcc act ggt gct ggg aag acc cac act atg cta gga tca gct gat	384
62	Gly Ala Thr Gly Ala Gly Lys Thr His Thr Met Leu Gly Ser Ala Asp	
63	115 120 125	

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65 gaa cct gga gtg atg tat cta aca atg tta cac ctt tac aaa tgc atg	432
66 Glu Pro Gly Val Met Tyr Leu Thr Met Leu His Leu Tyr Lys Cys Met	
67 130 135 140	
69 gag att aaa gaa gag aaa ata tgt agt act gca gtt tca tat ctg	480
70 Asp Glu Ile Lys Glu Glu Lys Ile Cys Ser Thr Ala Val Ser Tyr Leu	
71 145 150 155 160	
73 gag gta tat aat gaa cag att cgt gat ctc tta gta aat tca ggg cca	528
74 Glu Val Tyr Asn Glu Gln Ile Arg Asp Leu Leu Val Asn Ser Gly Pro	
75 165 170 175	
77 ctt qct gtc cgg gaa gat acc caa aaa ggg qtg gtc gtt cat gga ctt	576
78 Leu Ala Val Arg Glu Asp Thr Gln Lys Gly Val Val Val His Gly Leu	
79 180 185 190	
81 act tta cac cag ccc aaa tcc tca gaa gaa att tta cat tta ttg gat	624
82 Thr Leu His Gln Pro Lys Ser Ser Glu Glu Ile Leu His Leu Leu Asp	
83 195 200 205	
85 aat gga aac aaa aac agg aca caa cat ccc act gat atg aat gcc aca	672
86 Asn Gly Asn Lys Asn Arg Thr Gln His Pro Thr Asp Met Asn Ala Thr	
87 210 215 220	
89 tct tct cgt tct cat gct gtt ttc caa att tac ttg cga caa caa gac	720
90 Ser Ser Arg Ser His Ala Val Phe Gln Ile Tyr Leu Arg Gln Gln Asp	
91 225 230 235 240	
93 aaa aca gca agt atc aat caa aat gtc cgt att gcc aag atg tca ctc	768
94 Lys Thr Ala Ser Ile Asn Gln Asn Val Arg Ile Ala Lys Met Ser Leu	
95 245 250 255	
97 att gac ctg gca gga tct gag cga gca agt act tcc ggt gct aag ggg	816
98 Ile Asp Leu Ala Gly Ser Glu Arg Ala Ser Thr Ser Gly Ala Lys Gly	
99 260 265 270	
101 acc cga ttt gta gaa ggc aca aat att aat aga tca ctt tta gct ctt	864
102 Thr Arg Phe Val Glu Gly Thr Asn Ile Asn Arg Ser Leu Leu Ala Leu	
103 275 280 285	
105 ggg aat gtc atc aat gcc tta gca gat tca aag aga aag aat cag cat	912
106 Gly Asn Val Ile Asn Ala Leu Ala Asp Ser Lys Arg Lys Asn Gln His	
107 290 295 300	
109 atc cct tac aga aat agt aag ctt act cgc ttg tta aag gat tct ctt	960
110 Ile Pro Tyr Arg Asn Ser Lys Leu Thr Arg Leu Leu Lys Asp Ser Leu	
111 305 310 315 320	
113 gga gga aac tgt caa act ata atg ata gct gct gtt agt cct tcc tct	1008
114 Gly Gly Asn Cys Gln Thr Ile Met Ile Ala Ala Val Ser Pro Ser Ser	
115 325 330 335	
117 gta ttc tac gat gac aca tat aac act ctt aag tat gct aac cgg gca	1056
118 Val Phe Tyr Asp Asp Thr Tyr Asn Thr Leu Lys Tyr Ala Asn Arg Ala	
119 340 345 350	
121 aag gac att aaa tct tct ttg aag agc aat gtt ctt aat gtc aat aat	1104
122 Lys Asp Ile Lys Ser Ser Leu Lys Ser Asn Val Leu Asn Val Asn Asn	
123 355 360 365	
125 cat ata act caa tat gta aag atc tgt aat gag cag aag gca gag att	1152
126 His Ile Thr Gln Tyr Val Lys Ile Cys Asn Glu Gln Lys Ala Glu Ile	
127 370 375 380	
129 tta ttg tta aaa gaa aaa cta aaa gcc tat gaa gaa cag aaa gcc ttc	1200

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130	Leu	Leu	Leu	Lys	Glu	Lys	Leu	Lys	Ala	Tyr	Glu	Glu	Gln	Lys	Ala	Phe
131	385				390						395					400
133	act	aat	aat	gac	caa	gca	aag	tta	atg	att	tca	aac	cct	cag	gaa	
134	Thr	Asn	Glu	Asn	Asp	Gln	Ala	Lys	Leu	Met	Ile	Ser	Asn	Pro	Gln	Glu
135																415
137	aaa	gaa	atc	gaa	agg	ttt	caa	gaa	atc	ctg	aac	tgc	ttg	ttc	cag	aat
138	Lys	Glu	Ile	Glu	Arg	Phe	Gln	Glu	Ile	Leu	Asn	Cys	Leu	Phe	Gln	Asn
139																430
141	cga	gaa	gaa	att	aga	caa	gaa	tat	ctg	aag	ttg	gaa	atg	tta	ctt	aaa
142	Arg	Glu	Glu	Ile	Arg	Gln	Glu	Tyr	Leu	Lys	Leu	Glu	Met	Leu	Leu	Lys
143																445
145	gaa	aat	gaa	ctt	aaa	tca	ttc	tac	caa	caa	cag	tgc	cat	aaa	caa	ata
146	Glu	Asn	Glu	Leu	Lys	Ser	Phe	Tyr	Gln	Gln	Gln	Cys	His	Lys	Gln	Ile
147																460
149	gaa	atg	atg	tgt	tct	gaa	gac	aaa	gta	gaa	aag	gcc	act	gga	aaa	cga
150	Glu	Met	Met	Cys	Ser	Glu	Asp	Lys	Val	Glu	Lys	Ala	Thr	Gly	Lys	Arg
151																480
153	gat	cat	aga	ctt	gca	atg	ttg	aaa	act	cgt	cgc	tcc	tac	ctg	gag	aaa
154	Asp	His	Arg	Leu	Ala	Met	Leu	Lys	Thr	Arg	Arg	Ser	Tyr	Leu	Glu	Lys
155																495
157	agg	agg	gag	gaa	ttg	aag	caa	ttt	gat	gag	aat	act	aat	tgg	ctc	
158	Arg	Arg	Glu	Glu	Leu	Lys	Gln	Phe	Asp	Glu	Asn	Thr	Asn	Trp	Leu	
159																510
161	cat	cgt	gtc	gaa	aaa	gaa	atg	gga	ctc	tta	agt	caa	aac	ggt	cat	att
162	His	Arg	Val	Glu	Lys	Glu	Met	Gly	Leu	Leu	Ser	Gln	Asn	Gly	His	Ile
163																525
165	cca	aag	gaa	ctc	aag	aaa	gat	ctt	cat	tgt	cac	cat	ttg	cac	ctc	cag
166	Pro	Lys	Glu	Leu	Lys	Asp	Leu	His	Cys	His	His	Leu	His	Leu	Gln	
167																540
169	aac	aaa	gat	ttg	aaa	gca	caa	att	aga	cat	atg	atg	gat	cta	gct	tgt
170	Asn	Lys	Asp	Leu	Lys	Ala	Gln	Ile	Arg	His	Met	Met	Asp	Leu	Ala	Cys
171																560
173	ctt	cag	gaa	cag	caa	cac	agg	cag	act	gaa	gca	gta	ttg	aat	gct	tta
174	Leu	Gln	Glu	Gln	His	Arg	Gln	Thr	Glu	Ala	Val	Leu	Asn	Ala	Leu	
175																575
177	ctt	cca	acc	cta	aga	aaa	caa	tat	tgc	aca	tta	aaa	gaa	gcc	ggc	ctg
178	Leu	Pro	Thr	Leu	Arg	Lys	Gln	Tyr	Cys	Thr	Leu	Lys	Glu	Ala	Gly	Leu
179																590
181	tca	aat	gct	gct	ttt	gaa	tct	gac	ttc	aaa	gag	atc	gaa	cat	ttg	gta
182	Ser	Asn	Ala	Ala	Phe	Glu	Ser	Asp	Phe	Lys	Glu	Ile	Glu	His	Leu	Val
183																605
185	gag	agg	aaa	aaa	gtg	gta	gtt	tgg	gct	gac	caa	act	gcc	gaa	caa	cca
186	Glu	Arg	Lys	Lys	Val	Val	Val	Trp	Ala	Asp	Gln	Thr	Ala	Glu	Gln	Pro
187																620
189	aag	caa	aac	gat	cta	cca	ggg	att	tct	gtt	atc	acc	ttt	cca	caa	
190	Lys	Gln	Asn	Asp	Leu	Pro	Gly	Ile	Ser	Val	Leu	Met	Thr	Phe	Pro	Gln
191																640
193	ctt	gga	cca	gtt	cag	cct	att	cct	tgt	tgc	tca	tct	tca	ggt	gga	act
194	Leu	Gly	Pro	Val	Gln	Pro	Ile	Pro	Cys	Cys	Ser	Ser	Ser	Gly	Gly	Thr

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195	645	650	655	
197 aat ctg gtt aag att cct aca gaa aaa aga act cgg aga aaa cta atg				2016
198 Asn Leu Val Lys Ile Pro Thr Glu Lys Arg Thr Arg Arg Lys Leu Met				
199	660	665	670	
201 cca tct ccc ttg aaa gga cag cat act cta aag tct cca cca tct caa				2064
202 Pro Ser Pro Leu Lys Gly Gln His Thr Leu Lys Ser Pro Pro Ser Gln				
203	675	680	685	
205 agt gtg cag ctc aat gat tct ctt agc aaa gaa ctt cag cct att gta				2112
206 Ser Val Gln Leu Asn Asp Ser Leu Ser Lys Glu Leu Gln Pro Ile Val				
207	690	695	700	
209 tat aca cca gaa gac tgt aga aaa gct ttt caa aat ccg tct aca gta				2160
210 Tyr Thr Pro Glu Asp Cys Arg Lys Ala Phe Gln Asn Pro Ser Thr Val				
211 705	710	715	720	
213 acc tta atg aaa cca tca tca ttt act aca agt ttt cag gct atc agc				2208
214 Thr Leu Met Lys Pro Ser Ser Phe Thr Thr Ser Phe Gln Ala Ile Ser				
215	725	730	735	
217 tca aac ata aac agt gat aat tgt ctg aaa atg ttg tgt gaa gta gct				2256
218 Ser Asn Ile Asn Ser Asp Asn Cys Leu Lys Met Leu Cys Glu Val Ala				
219	740	745	750	
221 atc cct cat aat aga aga aaa gaa tgt gga cag gag gac ttg gac tct				2304
222 Ile Pro His Asn Arg Arg Lys Glu Cys Gly Gln Glu Asp Leu Asp Ser				
223	755	760	765	
225 aca ttt act ata tgt gaa gac atc aag agc tcg aag tgt aaa tta ccc				2352
226 Thr Phe Thr Ile Cys Glu Asp Ile Lys Ser Ser Lys Cys Lys Leu Pro				
227	770	775	780	
229 gaa caa gaa tca cta cca aat gat aac aaa gac att tta caa cgg ctt				2400
230 Glu Gln Glu Ser Leu Pro Asn Asp Asn Lys Asp Ile Leu Gln Arg Leu				
231 785	790	795	800	
233 gat cct tct tca ttc tca act aag cat tct atg cct gta cca agc atg				2448
234 Asp Pro Ser Ser Phe Ser Thr Lys His Ser Met Pro Val Pro Ser Met				
235	805	810	815	
237 gtg cca tcc tac atg gca atg act act gct gcc aaa agg aaa cgg aaa				2496
238 Val Pro Ser Tyr Met Ala Met Thr Thr Ala Ala Lys Arg Lys Arg Lys				
239	820	825	830	
241 tta aca agt tct aca tca aac agt tcg tta act gca gac gta aat tct				2544
242 Leu Thr Ser Ser Thr Ser Asn Ser Ser Leu Thr Ala Asp Val Asn Ser				
243	835	840	845	
245 gga ttt gcc aaa cgt gtt cga caa gat aat tca agt gag aag cac tta				2592
246 Gly Phe Ala Lys Arg Val Arg Gln Asp Asn Ser Ser Glu Lys His Leu				
247	850	855	860	
249 caa gaa aac aaa cca aca atg gaa cat aaa aga aac atc tgt aaa ata				2640
250 Gln Glu Asn Lys Pro Thr Met Glu His Lys Arg Asn Ile Cys Lys Ile				
251 865	870	875	880	
253 aat cca agc atg gtt aga aaa ttt gga aga aat att tca aaa gga aat				2688
254 Asn Pro Ser Met Val Arg Lys Phe Gly Arg Asn Ile Ser Lys Gly Asn				
255	885	890	895	
257 cta aga taa				2697
258 Leu Arg				
262 <210> SEQ ID NO: 2				

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263 <211> LENGTH: 898
 264 <212> TYPE: PRT
 265 <213> ORGANISM: Homo sapiens
 267 <400> SEQUENCE: 2
 268 Met Ser Val Thr Glu Glu Asp Leu Cys His His Met Lys Val Val Val
 269 1 5 10 15
 270 Arg Val Arg Pro Glu Asn Thr Lys Glu Lys Ala Ala Gly Phe His Lys
 271 20 25 30
 272 Val Val His Val Val Asp Lys His Ile Leu Val Phe Asp Pro Lys Gln
 273 35 40 45
 274 Glu Glu Val Ser Phe Phe His Gly Lys Lys Thr Thr Asn Gln Asn Val
 275 50 55 60
 276 Ile Lys Lys Gln Asn Lys Asp Leu Lys Phe Val Phe Asp Ala Val Phe
 277 65 70 75 80
 278 Asp Glu Thr Ser Thr Gln Ser Glu Val Phe Glu His Thr Thr Lys Pro
 279 85 90 95
 280 Ile Leu Arg Ser Phe Leu Asn Gly Tyr Asn Cys Thr Val Leu Ala Tyr
 281 100 105 110
 282 Gly Ala Thr Gly Ala Gly Lys Thr His Thr Met Leu Gly Ser Ala Asp
 283 115 120 125
 284 Glu Pro Gly Val Met Tyr Leu Thr Met Leu His Leu Tyr Lys Cys Met
 285 130 135 140
 286 Asp Glu Ile Lys Glu Glu Lys Ile Cys Ser Thr Ala Val Ser Tyr Leu
 287 145 150 155 160
 288 Glu Val Tyr Asn Glu Gln Ile Arg Asp Leu Leu Val Asn Ser Gly Pro
 289 165 170 175
 290 Leu Ala Val Arg Glu Asp Thr Gln Lys Gly Val Val Val His Gly Leu
 291 180 185 190
 292 Thr Leu His Gln Pro Lys Ser Ser Glu Glu Ile Leu His Leu Leu Asp
 293 195 200 205
 294 Asn Gly Asn Lys Asn Arg Thr Gln His Pro Thr Asp Met Asn Ala Thr
 295 210 215 220
 296 Ser Ser Arg Ser His Ala Val Phe Gln Ile Tyr Leu Arg Gln Gln Asp
 297 225 230 235 240
 298 Lys Thr Ala Ser Ile Asn Gln Asn Val Arg Ile Ala Lys Met Ser Leu
 299 245 250 255
 300 Ile Asp Leu Ala Gly Ser Glu Arg Ala Ser Thr Ser Gly Ala Lys Gly
 301 260 265 270
 302 Thr Arg Phe Val Glu Gly Thr Asn Ile Asn Arg Ser Leu Leu Ala Leu
 303 275 280 285
 304 Gly Asn Val Ile Asn Ala Leu Ala Asp Ser Lys Arg Lys Asn Gln His
 305 290 295 300
 306 Ile Pro Tyr Arg Asn Ser Lys Leu Thr Arg Leu Leu Lys Asp Ser Leu
 307 305 310 315 320
 308 Gly Gly Asn Cys Gln Thr Ile Met Ile Ala Ala Val Ser Pro Ser Ser
 309 325 330 335
 310 Val Phe Tyr Asp Asp Thr Tyr Asn Thr Leu Lys Tyr Ala Asn Arg Ala
 311 340 345 350
 312 Lys Asp Ile Lys Ser Ser Leu Lys Ser Asn Val Leu Asn Val Asn Asn

VERIFICATION SUMMARY

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